

SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Regucalcin gene-transferred non-human animals

<130> YG2002-18PCT

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<150> JP P2001-287698

<151> 2001-9-20

<150> JP P2002-177666

<151> 2002-6-18

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 900

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(900)

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Met	Ser	Ser	Ile	Lys	Ile	Glu	Cys	Val	Leu	Arg	Glu	Asn	Tyr	Arg	Cys	
1				5				10					15			

ggg	gag	icc	ccg	gtg	tgg	gag	gag	gca	tca	aag	tgt	ctg	ctg	ttt	gta	96
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Gly	Glu	Ser	Pro	Val	Trp	Glu	Glu	Ala	Ser	Lys	Cys	Leu	Leu	Phe	Val		
20								25				30					
gac	atc	cct	tca	aag	act	gic	tgc	cga	tgg	gat	tcg	atc	agc	aat	cga	144	
Asp	Ile	Pro	Ser	Lys	Thr	Val	Cys	Arg	Trp	Asp	Ser	Ile	Ser	Asn	Arg		
35				40				45									
gtg	cag	cga	gtt	ggc	gta	gat	gcc	cca	gtc	agt	tca	gtg	gca	ctt	cga	192	
Val	Gln	Arg	Val	Gly	Val	Asp	Ala	Pro	Val	Ser	Ser	Val	Ala	Leu	Arg		
50				55				60									
cag	tca	gga	ggc	tat	gtt	gcc	acc	att	gga	acc	aag	ttc	tgt	gct	tig	240	
Gln	Ser	Gly	Gly	Tyr	Val	Ala	Thr	Ile	Gly	Thr	Lys	Phe	Cys	Ala	Leu		
65				70				75				80					
aac	tgg	gaa	gat	caa	tca	gta	ttt	atc	cta	gcc	atg	gtg	gat	gaa	gat	288	
Asn	Trp	Glu	Asp	Gln	Ser	Val	Phe	Ile	Leu	Ala	Met	Val	Asp	Glu	Asp		
85				90				95									
aag	aaa	aac	aat	cga	ttc	aat	gat	ggg	aag	gtg	gat	cct	gct	ggg	aga	336	
Lys	Lys	Asn	Asn	Arg	Phe	Asn	Asp	Gly	Lys	Val	Asp	Pro	Ala	Gly	Arg		
100				105				110									
tac	ttt	gct	ggt	acc	atg	gct	gag	gaa	acc	gcc	cca	gct	gtt	ctg	gag	384	
Tyr	Phe	Ala	Gly	Thr	Met	Ala	Glu	Glu	Thr	Ala	Pro	Ala	Val	Leu	Glu		
115				120				125									
cgg	cac	caa	ggg	tcc	ttg	tac	tcc	ctt	ttt	cct	gat	cac	agt	gtg	aag	432	
Arg	His	Gln	Gly	Ser	Leu	Tyr	Ser	Leu	Phe	Pro	Asp	His	Ser	Val	Lys		
130				135				140									
aaa	tac	ttt	aac	caa	gtg	gat	atc	tcc	aat	ggc	ttg	gat	tgg	tcc	ctg	480	
Lys	Tyr	Phe	Asn	Gln	Val	Asp	Ile	Ser	Asn	Gly	Leu	Asp	Trp	Ser	Leu		
145				150				155				160					
gac	cat	aaa	atc	ttc	tac	tac	att	gac	agc	cig	tcc	tac	act	gtg	gat	528	

Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp	
165 170 175	
gcc ttt gac tat gac ctg cca aca gga cag att tcc aac cgc agg act	576
Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr	
180 185 190	
glt tac aag atg gaa aaa gat gaa caa atc cca gat gga atg tgc att	624
Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile	
195 200 205	
gat gtt gag ggg aag ctt tgg gtg gcc tgt tac aat gga gga aga gta	672
Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val	
210 215 220	
att cgc cta gat cct gag aca ggg aaa aga ctg caa act gtg aag ttg	720
Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu	
225 230 235 240	
cct gtt gat aaa aca act tca tgc tgc ttt gga ggg aag gat tac tct	768
Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser	
245 250 255	
gaa atg tac gtg aca tgt gcc agg gat ggg atg agc gcc gaa ggt ctt	816
Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu	
260 265 270	
ttg agg cag cct gat gct ggt aac att ttc aag ata aca ggt ctt ggg	864
Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly	
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Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly	
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 Asp Ile Pro Ser Lys Thr Val Cys Arg Trp Asp Ser Ile Ser Asn Arg
 35 40 45
 Val Gln Arg Val Gly Val Asp Ala Pro Val Ser Ser Val Ala Leu Arg
 50 55 60
 Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
 65 70 75 80
 Asn Trp Glu Asp Gln Ser Val Phe Ile Leu Ala Met Val Asp Glu Asp
 85 90 95
 Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
 100 105 110
 Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
 115 120 125
 Arg His Gln Gly Ser Leu Tyr Ser Leu Phe Pro Asp His Ser Val Lys
 130 135 140
 Lys Tyr Phe Asn Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
 145 150 155 160
 Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp
 165 170 175
 Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr
 180 185 190
 Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile
 195 200 205
 Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
 210 215 220
 Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
 225 230 235 240

Pro	Val	Asp	Lys	Thr	Thr	Ser	Cys	Cys	Phe	Gly	Gly	Lys	Asp	Tyr	Ser
				245					250					255	
Glu	Met	Tyr	Val	Thr	Cys	Ala	Arg	Asp	Gly	Met	Ser	Ala	Glu	Gly	Leu
			260					265					270		
Leu	Arg	Gln	Pro	Asp	Ala	Gly	Asn	Ile	Phe	Lys	Ile	Thr	Gly	Leu	Gly
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Val	Lys	Gly	Ile	Ala	Pro	Tyr	Ser	Tyr	Ala	Gly					
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer huRC-1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer huRC-2

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23